

The Dynamics of Vector-Borne Relapsing Diseases

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Abstract

In this paper we describe the dynamics of a vector-borne relapsing disease, such as tick-borne relapsing fever, using the methods of compartmental models. After some motivation, model description, and a brief overview of the theory of compartmental models, we compute a general form of the reproductive ratio R_0 , which is the average number of new infections produced by a single infected individual. A disease free equilibrium undergoes a bifurcation at $R_0 = 1$ and we show that for an arbitrary number of relapses it is a transcritical bifurcation with a single branch of endemic equilibria that is locally asymptotically stable for R_0 sufficiently close to 1. We then show that these results can be extended to a variant of the model that allows for variation in the number of relapses before recovery. We close with some discussion and directions for future research.

1 Introduction

Many mathematical models dealing with the spread of infectious diseases show a rich variety of dynamics that arise from various nonlinear interactions or temporal forcing e.g. [15]. Vector-borne diseases are additionally complex with interactions between host and vector species [6]. Tick-borne relapsing fever (TBRF) is an example of a system that incorporates such complex interactions in a multiple host-vector community.

In North America, TBRF is caused by several species of spiral-shaped bacteria (*Borrelia* spp.) that are transmitted to their hosts through the bite of an infected vector, the soft ticks of the genus *Ornithodoros*. Once infected with the bacteria, ticks remain infectious for extended periods and possibly for life [14]. Most human cases occur in the summer months and are often associated with sleeping in rustic cabins in mountainous areas of the Western United States [7]. The model presented in this paper is motivated by a system located on Wild Horse Island, Flathead Lake, Lake County, Montana (WHI), where the presence of this pathogen has been confirmed [22]. The island harbors two host species, the red squirrel (*Tamiasciurus hudsonicus*) and the deer mouse (*Peromyscus maniculatus*) and a single vector species (*O. hermsi*), which is thought to control the disease patterns on the island. See [14] for more details.

Compartmental models, such as the SIR models with susceptible, infectious, and removed compartments, have been applied to many disease and disease-like systems in an effort to examine system dynamics [8, 9, 16, 18, 19, 21, 24, 26]. In these epidemic models, susceptible individuals pass into the infected class and then transition to the removed class. For some diseases, recovered individuals may relapse through a reactivation of infection and revert back to an infected class. TBRF is a system in which relapse always occurs, but between different infected classes caused by

the bacteria's antigenic variation [4]. The advantage of antigenic variation is to extend the length of infection so that the host will still be infected at the next interaction with a susceptible vector [1, 10]. The question that we raise is how the dynamics of the spread of the disease are affected by the number of relapses, and how do these dynamics differ from a vector-borne disease with no relapses.

Given a mathematical model for disease spread, the disease reproduction number, R_0 , is an essential summary parameter. It is defined as the average number of secondary infections produced when one infected individual is introduced into a host population in which all individuals are susceptible [5]. When $R_0 < 1$, the disease free equilibrium (DFE), at which the population remains in the absence of disease, is locally asymptotically stable. However, if $R_0 > 1$, then the DFE is unstable and invasion is always possible [11] and a new endemic equilibrium (EE) exists.

A key assumption for the host-vector disease modeling is the definition of the transmission term, which represents the contact between hosts and vectors. The formulation of the transmission term directly affects the reproduction number R_0 . For host-vector disease models, the transmission term includes vector biting rate f , which controls the disease transmission both from the vector-to-host and from the host-to-vector. The TBRF model follows frequency-dependent transmission assumptions through the biting rate, since a blood meal is required only once every three months regardless of the host population density. Following this framework, it is reasonable to assume that a host would experience an increasing number of bites as the vector population increased [14]. While our work here shares techniques with previous work done on staged progression models [9, 12, 13], the key difference is the addition of vectors.

In this paper we derive a general form for R_0 when there is a single host species in the system, following the methodology of van den Dreissche and Watmough for general compartmental disease models [23] which is then extended with an arbitrary number of relapsing states. From this we show how R_0 depends on the number of relapses and the various parameters in the model. We then classify the bifurcation at $R_0 = 1$, showing that it is transcritical with an exchange of stability between a disease free equilibrium and an endemic equilibrium. We also show that there is a unique endemic equilibrium for each value of $R_0 > 1$. We finally consider a variation of the model which accounts for differing number of relapses before recovery, and close with discussion and future work.

2 Single Host Vector Model

To begin constructing the model we first make assumptions motivated by the spread of TBRF on WHI. We assume that new infections only occur when an infected vector bites a susceptible host or when a susceptible vector bites an infected host. We also assume that when a vector becomes infected, it is infected for life. Furthermore, we assume that the transmission terms are frequency dependent through the biting rate f . The infected hosts relapse into infected compartments sequentially at a rate α_i and recover from the disease at rate γ . The total populations of hosts and vectors are assumed to remain constant are denoted by N and \tilde{N} respectively (throughout the paper we will indicate quantities corresponding to the vectors with a \sim). Though the death rates may vary among the different infected compartments, we will require that recruitment (reproduction) and death rates are equal. In more precise terms, we assume that the dynamics occur on an invariant hyperplane. This assumption greatly simplifies the model, as will be seen shortly. Although it appears at first to be a restrictive assumption, it is a natural for determining R_0 , where it is often assumed that the disease is spreading among a population large enough that the net change is essentially zero.

The infection dynamics in a single host-vector system with $j - 1$ relapsing rates for $j \geq 1$ infected compartments involve the number of susceptible hosts $S(t)$, infectious hosts $I_k(t)$, removed hosts $R(t)$, susceptible vectors $\tilde{S}(t)$, and infected vectors $\tilde{I}(t)$, where the total host population is $N = S + \sum_{k=1}^j I_k + R$ and the total vector population $\tilde{N} = \tilde{S} + \tilde{I}$. A conceptual model for this scheme is given in Figure 2.1. The equations for the model are as follows: first the host equations

$$\begin{aligned}
S' &= \beta(N) - fc_v \tilde{I} \frac{S}{N} - \mu_s S, \\
I_1' &= fc_v \tilde{I} \frac{S}{N} - \alpha_1 I_1 - \mu_1 I_1, \\
I_2' &= \alpha_1 I_1 - \alpha_2 I_2 - \mu_2 I_2, \\
&\vdots \\
I_{j-1}' &= \alpha_{j-2} I_{j-2} - \alpha_{j-1} I_{j-1} - \mu_{j-1} I_{j-1}, \\
I_j' &= \alpha_{j-1} I_{j-1} - \gamma I_j - \mu_j I_j, \\
R' &= \gamma I_j - \mu_r R,
\end{aligned} \tag{2.1}$$

and the vector equations:

$$\begin{aligned}
\tilde{S}' &= \beta_v(\tilde{N}, N) - \frac{fc\tilde{S}}{N} \sum_{k=1}^j I_k - \tilde{\mu}_s \tilde{S}, \\
\tilde{I}' &= \frac{fc\tilde{S}}{N} \sum_{k=1}^j I_k - \tilde{\mu} \tilde{I}.
\end{aligned} \tag{2.2}$$

The growth rates β and β_v are logistic, given as follows:

$$\begin{aligned}
\beta(N) &= \beta_1 N - \left(\frac{\beta_1 - \mu_s}{\bar{S}} \right) N^2, \\
\beta_v(\tilde{N}, N) &= \beta_{v1} \tilde{N} N - \left(\frac{\beta_{v1} \bar{S} - \tilde{\mu}_s}{\bar{S}_v} \right) \tilde{N}^2.
\end{aligned}$$

We insist that $\beta_1 \geq \mu_s$ and $\beta_{v1} \geq \tilde{\mu}_s$, for these to be well defined. Further details regarding this being a well defined model are found in Appendix A.1, where we show that the system satisfies the conditions laid out in [23]. Here \bar{S} and \bar{S}_v are constants. It is then easy to see that

$$(S, I_1, \dots, I_j, R, \tilde{S}, \tilde{I}) = (\bar{S}, 0, \dots, \bar{S}_v, 0)$$

is a fixed point of the system. This is known as the Disease Free Equilibrium (DFE). To investigate the stability of the DFE we calculate R_0 for arbitrary j . We will make the natural assumptions in this model that $\mu_i \geq \mu_s$, $\mu_r \geq \mu_s$, and that $\tilde{\mu} \geq \tilde{\mu}_s$. We are assuming that having the disease will only serve to increase the death rate over the susceptible population. This leads to the following result:

Proposition 1. *The manifold $N = \bar{S}$ is invariant if and only if $\mu_s = \mu_i$ and $\mu_s = \mu_r$*

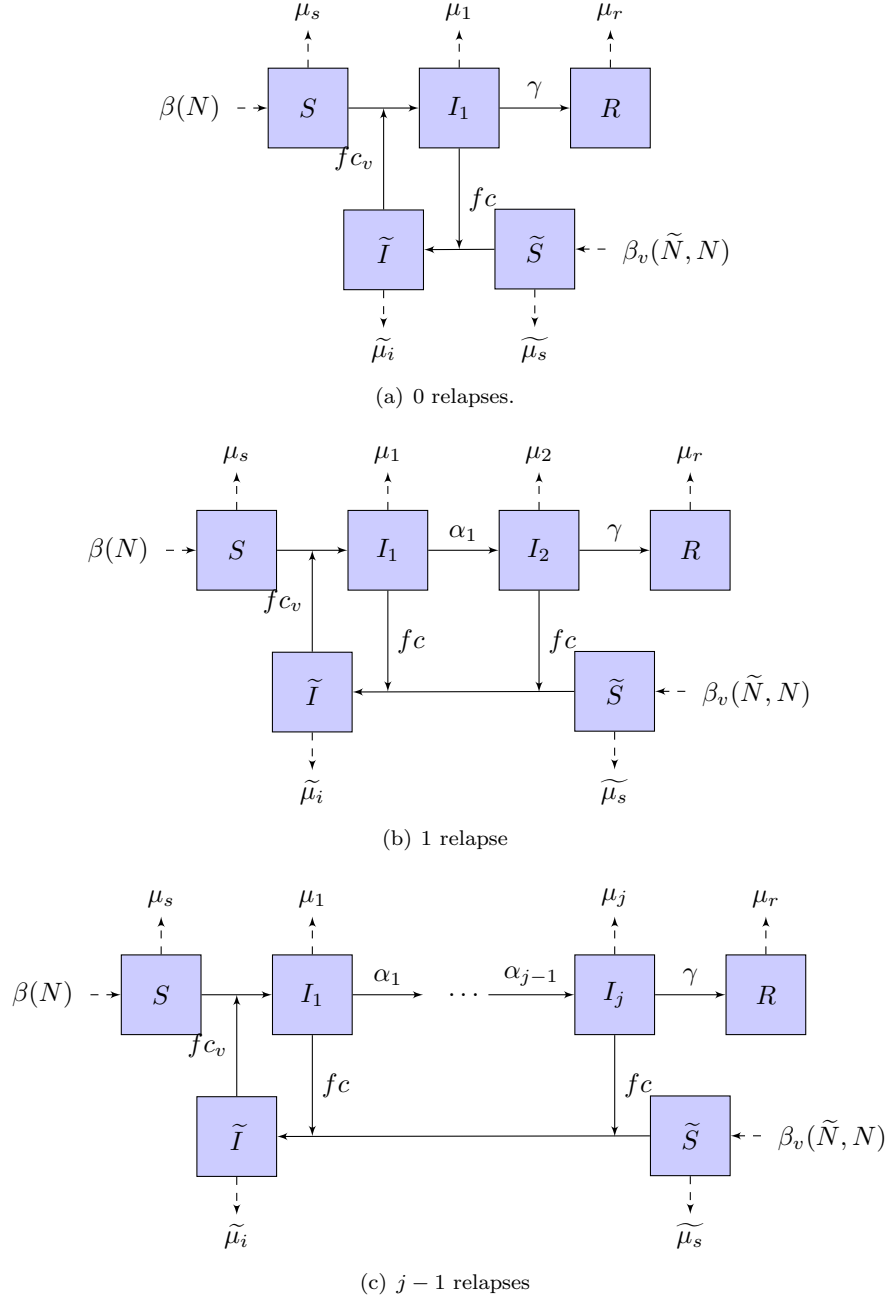


Figure 2.1: Conceptual models for the cross-infection dynamics between a single host-vector system, which includes (a) no relapses between $j = 1$ infected compartments, (b) 1 relapse between $j = 2$ infected compartments, and (c) $j - 1$ relapses between j infected compartments. Dashed lines are the vital rates for each population, where solid lines refer to interaction rates between compartments.

Variable	Definition	Dimensionless Form
N	Total host population.	n
\tilde{N}	Total vector population.	\tilde{n}
S	Susceptible hosts.	s
I_k	Hosts in the k^{th} infected compartment.	i_k
R	Recovered hosts.	r
\tilde{S}	Susceptible vectors.	\tilde{s}
\tilde{I}	Infected vectors.	\tilde{i}

Parameter	Definition	Dimensionless Form
f	Biting Rate.	
c_v	Vector Competency.	
μ_s	Susceptible Death Rate.	b_s
α_k	Transfer rate from the k^{th} infected compartment.	q_k
μ_k	Death rate in the k^{th} infected compartment.	b_k
γ	Rate of recovery.	1
μ_r	Death rate of recovered individuals.	b_r
c	Host competency.	
$\tilde{\mu}_s$	Death rate of susceptible vectors.	\tilde{b}_s
$\tilde{\mu}$	Death rate of infected vectors.	\tilde{b}

Table 1: Variables and parameters for the model, with dimensionless forms where relevant. All parameters are positive.

Proof. First suppose that $\mu_s = \mu_i$ and $\mu_s = \mu_r$. Substituting this into the system and summing the equations yields

$$N' = \beta(N) - \mu_s N = \beta_1 N - \frac{(\beta_1 - \mu_s)N^2}{\bar{S}} - \mu_s N = (\beta_1 - \mu_s)N \left(1 - \frac{N}{\bar{S}}\right)$$

From this we can see if $N(0) = \bar{S}$, then $N(t) = \bar{S}$, and $N = \bar{S}$ is invariant.

Now assume that $N = \bar{S}$ is invariant. Then if $N(0) = \bar{S}$, N is constant and the first equation reduces to

$$S' = \mu_s(\bar{S} - S) - \frac{f c_v \tilde{I} S}{\bar{S}}$$

Then, summing the equations gives that

$$N' = \mu_s S + \sum_{k=1}^j \mu_k I_k + \mu_r R - \mu_s \bar{S}$$

But since N is constant, $N' = 0$, and we use the fact that $s + \sum I_k + R = \bar{S}$ so the above equation becomes

$$0 = \sum \left(\frac{\mu_i}{\mu_s} - 1 \right) I_k + \left(\frac{\mu_r}{\mu_s} - 1 \right) R$$

Now, $I_k, R \geq 0$, and since $\mu_i \geq \mu_s$ and $\mu_r \geq \mu_s$ we have

$$\frac{\mu_i}{\mu_s} \geq 1 \text{ and } \frac{\mu_r}{\mu_s} \geq 1$$

Since each term is nonnegative, the only way the sum can add to zero is if each term is zero. Since I_k and R can, at some time, be nonzero we must have $\frac{\mu_i}{\mu_s} - 1 = 0$ and $\frac{\mu_r}{\mu_s} - 1 = 0$. Thus $\mu_s = \mu_i = \mu_r$. \square

When the death rates are equal the host population has simple logistic dynamics:

$$N' = (\beta_1 - \mu_s)N \left(1 - \frac{N}{\bar{S}} \right)$$

In particular, if $\beta_1 > \mu_s$ we have $N = \bar{S}$ is an attracting fixed point. We can then apply the results from Chapter 2 of [17]: a fixed point that is asymptotically stable on the manifold $N = \bar{S}$ is asymptotically stable in the off-manifold dynamics. This will be relevant to our discussion of endemic equilibria in Section 4. The equality of the death rates is equivalent to the invariance of the manifolds $N = \bar{S}$ and $\tilde{N} = \bar{S}_v$, and restriction to these manifolds yields a simplification of the growth terms:

$$\beta(\bar{S}) = \mu_s \bar{S} \text{ and } \beta_v(\bar{S}_v, \bar{S}) = \tilde{\mu}_s \bar{S}_v$$

3 R_0 for the single host-vector system with $j - 1$ relapses.

3.1 Dimensionless Form

To ease some calculation we will put equations (2.1) and (2.2) in dimensionless form. Letting $\tau = \gamma t$, and scaling all the population variables by the corresponding initial total populations $N(0)$ and $\tilde{N}(0)$ gives the dimensionless form.

$$\begin{aligned} \frac{ds}{d\tau} &= \frac{\beta(N)}{\gamma N(0)} - k\tilde{i}\frac{s}{n} - b_s s \\ \frac{di_i}{d\tau} &= k\tilde{i}\frac{s}{n} - q_1 i_1 - b_1 i_1 \\ \frac{di_2}{d\tau} &= q_1 i_1 - q_2 i_2 - b_2 i_2 \\ &\vdots \\ \frac{di_{j-1}}{d\tau} &= q_{j-2} i_{j-2} - q_{j-1} i_{j-1} - b_{(j-1)} i_{j-1} \\ \frac{di_j}{d\tau} &= q_{j-1} i_{j-1} - i_j - b_j i_j \end{aligned}$$

$$\begin{aligned}\frac{dr}{d\tau} &= i_j - b_r r \\ \frac{d\tilde{s}}{d\tau} &= \frac{\beta_v(\tilde{N}, N)}{\gamma \tilde{N}(0)} - \frac{l\tilde{s}}{n} \sum_{m=1}^j i_m - \tilde{b}_s s_v \\ \frac{d\tilde{i}}{d\tau} &= \frac{l\tilde{s}}{n} \sum_{m=1}^j i_m - \tilde{b}_i \tilde{i}\end{aligned}$$

where $k = fc_v/\gamma$ and $l = fc/\gamma$.

3.2 General form for R_0

Following [23], we consider the reduced equations

$$\frac{d}{d\tau} \begin{bmatrix} i_1 \\ i_2 \\ \vdots \\ i_{j-1} \\ i_j \\ \tilde{i} \end{bmatrix} = \begin{bmatrix} k\tilde{i}\frac{s}{n} \\ 0 \\ \vdots \\ 0 \\ 0 \\ \frac{l\tilde{s}}{n} \sum_{k=1}^j i_k \end{bmatrix} - \begin{bmatrix} q_1 i_1 + b_1 i_1 \\ -q_1 i_1 + q_2 i_2 + b_2 i_2 \\ \vdots \\ -q_{j-2} i_{j-2} + q_{j-1} i_{j-1} + b_{j-1} i_{j-1} \\ -q_{j-1} i_{j-1} + i_j + b_j i_j \\ \tilde{b}_i \tilde{i} \end{bmatrix} = \mathbf{w} - \mathbf{v}$$

Next we take the Jacobian of \mathbf{w} and \mathbf{v} and evaluate them at the disease free equilibrium in order to find the matrices W and V , i.e.

$$W = \left[\begin{array}{cccc} 0 & \dots & 0 & k\frac{s}{n} \\ 0 & \dots & 0 & 0 \\ \vdots & & \vdots & \vdots \\ \frac{l\tilde{s}}{n} & \dots & \frac{l\tilde{s}}{n} & 0 \end{array} \right] \Big|_{DFE}$$

At the DFE we note that the entire host and vector populations are susceptible and there are no hosts in any of the relapse states. This means that $n = s = \bar{s}$ and $\tilde{n} = \tilde{s} = \bar{s}_v$ (the carrying capacities of each population). Hence

$$W = \begin{bmatrix} 0 & \dots & 0 & k \\ 0 & \dots & 0 & 0 \\ \vdots & & \vdots & \vdots \\ \frac{l\bar{s}_v}{\bar{s}} & \dots & \frac{l\bar{s}_v}{\bar{s}} & 0 \end{bmatrix}$$

For V , we note that the Jacobian is made up of constant values, namely

$$V = \begin{bmatrix} q_1 + b_1 & 0 & 0 & \dots & 0 & 0 & 0 & 0 \\ -q_1 & q_2 + b_2 & 0 & \dots & 0 & 0 & 0 & 0 \\ 0 & -q_2 & q_3 + b_3 & \dots & 0 & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & -q_{j-2} & q_{j-1} + b_{j-1} & 0 & 0 \\ 0 & 0 & 0 & \dots & 0 & -q_{j-1} & 1 + b_j & 0 \\ 0 & 0 & 0 & \dots & 0 & 0 & 0 & \widetilde{b_i} \end{bmatrix}$$

Clearly the matrix V is invertible (lower triangular, nonzero diagonal elements), although computing such an inverse is nontrivial. However, all we require is the dominant eigenvalue of WV^{-1} . Because W is fairly sparse we will not need to know all the entries of V^{-1} to extract it. Also, note that W and V are both $(j+1) \times (j+1)$ matrices.

The action of W on V^{-1} is to multiply the last row by k , make middle rows 0, and sum the first j elements of each columns and multiply it by the constant $\rho = \frac{ls_v}{s}$. Let us denote the elements of the last row of V^{-1} by ϵ_k and the sums of the first j elements of the k th column as δ_k . WV^{-1} then has a relatively simple form

$$WV^{-1} = \begin{bmatrix} k\epsilon_1 & \dots & k\epsilon_{j+1} \\ 0 & \dots & 0 \\ \vdots & & \vdots \\ 0 & \dots & 0 \\ \rho\delta_1 & \dots & \rho\delta_{j+1} \end{bmatrix}$$

From here we can move ahead with the eigenvalue calculation. This involves computing the determinant of

$$WV^{-1} - \lambda I = \begin{bmatrix} k\epsilon_1 - \lambda & k\epsilon_2 & \dots & k\epsilon_{j+1} \\ 0 & -\lambda & \dots & 0 \\ \vdots & \vdots & & \vdots \\ 0 & 0 & \dots & 0 \\ \rho\delta_1 & \rho\delta_2 & \dots & \rho\delta_{j+1} - \lambda \end{bmatrix}$$

Expanding along the first column we have

$$\det(WV^{-1} - \lambda I) = (k\epsilon_1 - \lambda) \cdot \det \begin{bmatrix} -\lambda & 0 & \dots & 0 \\ \vdots & \vdots & \vdots & \vdots \\ \rho\delta_2 & \rho\delta_3 & \dots & \rho\delta_{j+1} - \lambda \end{bmatrix} \\ + (-1)^{j+2} \rho\delta_1 \cdot \det \begin{bmatrix} k\epsilon_2 & \dots & k\epsilon_j & k\epsilon_{j+1} \\ -\lambda & \dots & 0 & 0 \\ \vdots & & \vdots & \vdots \\ 0 & \dots & -\lambda & 0 \end{bmatrix}$$

Computing the determinants in this expression is straightforward, noting that both are $j \times j$ matrices and the first is a lower triangular matrix, and thus the determinant is the product of the diagonal elements $(-\lambda)^{j-1}(\rho\delta_{j+1} - \lambda)$. For the second we expand along the last column to see that the determinant is

$$(-1)^{j+1} k\epsilon_{j+1} \cdot \det(-\lambda I) = (-1)^{j+1} k\epsilon_{j+1} (-\lambda)^{j-1}$$

Hence

$$\det(WV^{-1} - \lambda I) = (k\epsilon_1 - \lambda)(-\lambda)^{j-1}(\rho\delta_{j+1} - \lambda) \\ + (-1)^{j+2} \rho\delta_1 (-1)^{j+1} k\epsilon_{j+1} (-\lambda)^{j-1}$$

Hence, the characteristic polynomial only involves ϵ_1 , ϵ_{j+1} , δ_1 and δ_{j+1} , and we need only know the first and last column of V^{-1} . These can be computed by looking at the first and last row of the cofactor matrix. For ϵ_1 we look at the minor of $v_{j+1,1}$, and note the top row is all 0's, so that the minor, and thus the cofactor are 0 and thus $\epsilon_1 = 0$. To find δ_{j+1} we must find the cofactors of the first j elements on the bottom row of V , but when the bottom row is eliminated to compute the cofactor, the last column is all 0's, and hence each of the cofactors is 0. Thus $\delta_{j+1} = 0$. The characteristic polynomial then reduces to

$$(-\lambda)^{j-1} \lambda^2 - (-\lambda)^{j-1} \rho k \delta_1 \epsilon_{j+1}$$

Setting this equal to 0 and factoring:

$$\lambda = \pm \sqrt{\rho k \delta_1 \epsilon_{j+1}}$$

We have reduced finding the largest magnitude eigenvalue to computing the last element of the last column of V^{-1} (ϵ_{j+1}) and the sum of the first j elements in the first column of V^{-1} (δ_1). The elements of V^{-1} are not difficult to find, see [9].

If we define $q_0 = 1$ and $q_j = 1$ then

$$\delta_1 = \sum_{k=1}^j \frac{\prod_{\ell=0}^{k-1} q_\ell}{\prod_{\ell=1}^k (q_\ell + b_\ell)} = \sum_{k=1}^j \prod_{\ell=1}^k \frac{q_{\ell+1}}{q_\ell + b_\ell}$$

We can rewrite this sum as

$$\delta_1 = \frac{1}{q_1 + b_1} \left(1 + \frac{q_1}{q_2 + b_2} \left(1 + \frac{q_2}{q_3 + b_3} \left(1 + \dots \frac{q_{j-2}}{q_{j-1} + b_{j-1}} \left(1 + \frac{q_{j-1}}{1 + b_j} \right) \dots \right) \right) \right)$$

This gives that

$$R_0 = \sqrt{\frac{\rho k}{\tilde{b}_i} \frac{1}{q_1 + b_1} \left(1 + \frac{q_1}{q_2 + b_2} \left(1 + \frac{q_2}{q_3 + b_3} \left(1 + \dots \frac{q_{j-2}}{q_{j-1} + b_{j-1}} \left(1 + \frac{q_{j-1}}{1 + b_j} \right) \dots \right) \right) \right)}$$

Recall $\rho = \frac{l\bar{S}_v}{\bar{S}}$. Moving out of dimensionless form, we find

$$R_0 = f \sqrt{\frac{cc_v \bar{S}_v}{\tilde{\mu} \bar{S}} \frac{1}{\alpha_1 + \mu_1} \left(1 + \frac{\alpha_1}{\alpha_2 + \mu_2} \left(1 + \frac{\alpha_2}{\alpha_3 + \mu_3} \left(1 + \dots \frac{\alpha_{j-2}}{\alpha_{j-1} + \mu_{j-1}} \left(1 + \frac{\alpha_{j-1}}{\gamma + \mu_j} \right) \dots \right) \right) \right)}$$

This is the form that was conjectured in [14]. Alternatively,

$$R_0 = f \sqrt{\frac{cc_v \bar{S}_v}{\tilde{\mu} \bar{S}} \sum_{k=1}^j \prod_{l=1}^k \frac{\alpha_{l-1}}{\alpha_l + \mu_l}}$$

where $\alpha_0 = 1$ and $\alpha_j = \gamma$. This form best displays the dependence of R_0 on the number of relapses, $j - 1$. This is our first step in quantifying how the number of relapses affect the spread of a vector-borne disease.

Notice that R_0 is directly proportional to the biting rate f , the roots of the competencies c and c_v , and the root of the carrying capacity of the vector population. R_0 is inversely proportional to the death rate of the vectors $\tilde{\mu}$ and the carrying capacity of the host population \bar{S} . Thus R_0 can be completely controlled by these parameters. For instance, if the biting rate or the competencies are set to 0, the disease will eventually be eliminated from the population. Similarly, the higher the death rate of the vectors, the smaller R_0 will be, inhibiting the spread of the disease. It is also worth noting that R_0 only depends on the ratio of the vector and host populations sizes only. If the ratio of the populations is the same, R_0 is the same.

To investigate how R_0 depends on the transfer rates α_i , consider a model with $\mu_i = 0$. Then, letting $\beta = f \sqrt{\frac{cc_v \bar{S}_v}{\tilde{\mu} \bar{S}}}$, we have

$$\begin{aligned} R_0^2 &= \beta^2 \left(\frac{1}{\alpha_1} \left(1 + \frac{\alpha_1}{\alpha_2} \left(1 + \frac{\alpha_2}{\alpha_3} \left(1 + \dots \frac{\alpha_{j-2}}{\alpha_{j-1}} \left(1 + \frac{\alpha_{j-1}}{\alpha_j} \right) \dots \right) \right) \right) \right) \\ &= \beta^2 \left(\frac{1}{\alpha_1} + \frac{1}{\alpha_2} \left(1 + \frac{\alpha_2}{\alpha_3} \left(1 + \dots \frac{\alpha_{j-2}}{\alpha_{j-1}} \left(1 + \frac{\alpha_{j-1}}{\alpha_j} \right) \dots \right) \right) \right) \\ &= \beta^2 \left(\frac{1}{\alpha_1} + \frac{1}{\alpha_2} + \frac{1}{\alpha_3} \left(1 + \dots \frac{\alpha_{j-2}}{\alpha_{j-1}} \left(1 + \frac{\alpha_{j-1}}{\alpha_j} \right) \dots \right) \right) \end{aligned}$$

and so on, until

$$R_0^2 = \beta^2 \left(\frac{1}{\alpha_1} + \frac{1}{\alpha_2} + \frac{1}{\alpha_3} + \dots + \frac{1}{\alpha_{j-1}} + \frac{1}{\alpha_j} \right)$$

Let T_i be the average amount of time spent in the i th compartment, then $T_i \propto \frac{1}{\alpha_i}$, so that

$$R_0^2 \propto \beta^2 \sum T_i.$$

As the rates increase, the T_i will decrease and thus R_0 will decrease as well. Also, we can add relapses to the model but keep R_0 the same by fixing the total amount of time spent in the relapsing states. Thus, we can conclude that the addition of relapses to the model increases R_0 by increasing the amount of time that an infected host spends being infectious.

4 The Bifurcation at $R_0 = 1$.

We have already shown that there exists a bifurcation in the vector-borne relapsing disease model by finding a finite R_0 . We wish to learn more about the bifurcation. To do this we shall take advantage of center manifold theory. An introduction to such theory is written elsewhere [3, 25], but for our purposes it is enough to note that if the zero eigenvalue of the linear term is simple, then the dynamics on the center manifold are one dimensional. It is clear then that bifurcations with one simple zero eigenvalue are much simpler to study. We use this fact to investigate the stability of the EE near $R_0 = 1$. To do this, we insert a parameter μ into the equations where

$$\mu = 0 \iff R_0 = 1.$$

Define $\mu = R_0 - 1$ and so, solving for the biting rate:

$$f = \frac{\mu + 1}{\sqrt{\frac{cc_v \bar{S}_v}{\mu \bar{S}} \frac{1}{\alpha_1 + \mu_1} \left(1 + \frac{\alpha_1}{\alpha_2 + \mu_2} \left(1 + \frac{\alpha_2}{\alpha_3 + \mu_3} \left(1 + \dots \frac{\alpha_{j-2}}{\alpha_{j-1} + \mu_{j-1}} \left(1 + \frac{\alpha_{j-1}}{\gamma + \mu_j} \right) \dots \right) \right) \right)}}.$$

All other parameters being constant, we will abbreviate this as $f = \frac{\mu + 1}{\zeta}$. The Jacobian of the system at the DFE can be written in block form

$$\begin{pmatrix} F - V & 0 \\ -J_3 & -J_4 \end{pmatrix}.$$

Let v and w be the left and right eigenvectors corresponding to the eigenvalue 0. Without loss of generality we can choose these such that $vw = 1$. In the proof of Lemma 3 in [23] we see that we can also say that $v_i, w_i \geq 0$ for $1 \leq i \leq m$. Define

$$a = \sum_{i,j,k=1}^m v_i w_j w_k \left(\frac{1}{2} \frac{\partial^2 f_i}{\partial x_j \partial x_k}(x_0, 0) + \sum_{l=m+1}^n \varepsilon_{lk} \frac{\partial^2 f_i}{\partial x_j \partial x_l}(x_0, 0) \right),$$

$$b = \sum_{i,j=1}^n v_i w_j \frac{\partial^2 f_i}{\partial x_j \partial \mu}(x_0, 0),$$

where ε_{lk} , $l = m+1, \dots, n$, $k = 1, \dots, m$ are the $(l-m, k)$ entries of $-J_4^{-1} J_3$, when $R_0 = 1$. The following theorem is found in [23]

Theorem 1. *In a disease transmission model satisfying conditions 1-5, with the parameter μ as described above, with zero as a simple eigenvalue, and $b \neq 0$, there is a $\delta > 0$ such that*

- *if $a < 0$ then there are locally asymptotically stable endemic equilibria near x_0 for $0 < \mu < \delta$*

- if $a > 0$, then there are unstable endemic equilibria near x_0 for $-\delta < \mu < 0$.

The proof that 0 is a simple eigenvalue is found in Appendix A.2 and the proof for the following Lemma is found in Appendix A.3.

Lemma 1. $b \neq 0$, $a > 0$.

We can then apply Theorem 1 of [23] to our system, which states that there are asymptotically stable equilibria near the DFE when R_0 is sufficiently close to, but greater than 1.

5 Existence of Endemic Equilibria for all R_0

Having established the existence of branch of stable endemic equilibria (EE) near the bifurcation, there is a natural question regarding the behavior of these EE outside of the neighborhood of the bifurcation. Specifically, how does the local branch found in the previous section extends for larger (or smaller) values of R_0 . The complex form of R_0 and the arbitrary number of equations appear to make this problem quite difficult. But the majority of the equations have a simple linear form, and from these we can derive a simple recurrence relation for nontrivial equilibrium values of the I_2 through I_{j+1} in terms of I_1 . What remains is a fixed number of equations to solve. We thus make the following proposition

Proposition 2. *Given any $I_1 \geq 0$ there exist unique values $S, \tilde{S}, R, I_2, \dots, I_j$, and \tilde{I} such that*

$$S' = \tilde{S}' = R' = I_2' = \dots = I_j' = \tilde{I}' = 0.$$

Proof. Let I_1 be fixed. Consulting the equations for I_2 through I_{j-1} we see that

$$I_k' = 0 \iff I_k = \frac{\alpha_{k-1}I_{k-1}}{\alpha_k + \mu_k} = c_{k-1}I_{k-1} \text{ for } 2 \leq k \leq j-1.$$

For I_j

$$I_j' = 0 \iff I_j = \frac{\alpha_{j-1}I_{j-1}}{\gamma + \mu_j} = c_{j-1}I_{j-1},$$

and

$$R' = 0 \iff R = \frac{\gamma I_j}{\mu_r} = c_j I_j.$$

Then for I_2, \dots, I_j, R there is a simple multiplicative recurrence relation which is solved easily for I_k and R , namely

$$I_k = c_{k-1} \dots c_1 I_1; \quad R = c_k \dots c_1 I_1.$$

Thus the unique steady states for I_2, \dots, I_j and R are determined uniquely by I_1 . Now observe that at a steady state, inserting $c_0 = 1$,

$$\sum_{k=1}^j I_k = \sum_{k=1}^j c_{k-1} \dots c_0 I_1.$$

Let $\xi = \sum_{k=1}^j c_{k-1} \dots c_0$ and $\sum_{k=1}^j I_k = \xi I_1$. Then we have

$$\tilde{S}' = 0 \iff \tilde{\mu}_s(\bar{S}_v - \tilde{S}) - \frac{fc\tilde{S}}{\bar{S}}\xi I_1 = 0,$$

and thus

$$\tilde{S} = \frac{\tilde{\mu}_s \bar{S}_v}{\tilde{\mu}_s + \frac{fcI_1}{\bar{S}}\xi}.$$

So then \tilde{S} is uniquely determined by I_1 . Now, since $\tilde{I} = \bar{S}_v - \tilde{S}$, we should confirm that this value gives $\tilde{I}' = 0$ as follows.

$$\tilde{I}' = \frac{fc\tilde{S}I_1\xi}{\bar{S}} - \tilde{\mu}(\bar{S}_v - \tilde{S}) = \tilde{S} \left(\frac{fcI_1\xi}{\bar{S}} + \tilde{\mu} \right) - \tilde{\mu}_s \bar{S}_v,$$

but since $\tilde{\mu} = \tilde{\mu}_s$, and given the equilibrium value for \tilde{S} we have

$$\tilde{S} \left(\frac{fcI_1\xi}{\bar{S}} + \tilde{\mu}_s \right) - \tilde{\mu}_s \bar{S}_v = \tilde{\mu}_s \bar{S}_v - \tilde{\mu}_s \bar{S}_v = 0,$$

and I_1 uniquely determines the equilibrium value for \tilde{I} . Lastly we have

$$S' = 0 \iff S = \frac{\mu_s \bar{S}}{\mu_s + \frac{fc_v \tilde{I}}{\bar{S}}},$$

and as \tilde{I} is uniquely determined by I_1 , so is S . □

The consequence of this proposition is that the number of equilibrium points is determined by the number of values of I_1 such that $I_1' = 0$. Furthermore notice that $I_1 = 0$ implies that $S = \tilde{S} = R = I_2 = \dots = I_j = \tilde{I} = 0$, and we have generated the DFE. So we will only be looking for values such that $I_1 > 0$. We will also want to see how these values depend on R_0 , so it is useful to note the following form

$$R_0 = f \sqrt{\frac{cc_v \bar{S}_v}{\bar{S} \tilde{\mu}} \frac{1}{\alpha_1 + \mu_1}} \xi.$$

Now, $I_1' = 0$ if and only if

$$I_1(\alpha_1 + \mu_1) = \frac{fc_v \tilde{I} S}{\bar{S}}.$$

But since we also have $S' = 0$ this leads to

$$\frac{fc_v \tilde{I} S}{\bar{S}} = \mu_s(\bar{S} - S).$$

Thus

$$I_1 = \frac{\mu_s(\bar{S} - S)}{\alpha_1 + \mu_1} = \frac{\mu_s \bar{S}}{\alpha_1 + \mu_1} \left(1 - \frac{\mu_s}{\mu_s + \frac{fc_v \tilde{I}}{\bar{S}}} \right) = \frac{\mu_s \bar{S}}{\alpha_1 + \mu_1} \left(\frac{fc_v \tilde{I}}{\mu_s \bar{S} + fc_v \tilde{I}} \right).$$

Now, at an equilibria, we can write \tilde{I} uniquely in terms of I_1 :

$$\tilde{I} = \bar{S}_v - \tilde{S} = \bar{S}_v - \frac{\tilde{\mu}_s \bar{S}_v}{\tilde{\mu}_s + \frac{fcI_1}{\bar{S}} \xi} = \bar{S}_v \left(1 - \frac{\tilde{\mu}_s}{\tilde{\mu}_s + \frac{fcI_1}{\bar{S}} \xi} \right) = \frac{\bar{S}_v fcI_1 \xi}{\bar{S} \tilde{\mu}_s + fcI_1 \xi}.$$

Substituting this back into the expression for I_1 gives

$$I_1 = \frac{\mu_s \bar{S}}{\alpha_1 + \mu_1} \left(\frac{\bar{S}_v f^2 cc_v I_1 \xi}{\bar{S} \mu_s (\bar{S} \tilde{\mu}_s + fcI_1 \xi) + \bar{S}_v f^2 cc_v I_1 \xi} \right).$$

Because we are interested in solutions where $I_1 \neq 0$, we can divide both sides of the equation by I_1 and rearrange

$$\bar{S}^2 \mu_s \tilde{\mu}_s + fc \bar{S} \mu_s \xi I_1 + \bar{S}_v f^2 cc_v \xi I_1 = \frac{\mu_s \bar{S} \bar{S}_v f^2 cc_v \xi}{\alpha_1 + \mu_1}.$$

Thus

$$\begin{aligned} I_1 &= \frac{1}{fc \bar{S} \mu_s \xi + \bar{S}_v f^2 cc_v \xi} \left(\frac{\mu_s \bar{S} \bar{S}_v f^2 cc_v \xi}{\alpha_1 + \mu_1} - \bar{S}^2 \mu_s \tilde{\mu}_s \right) \\ &= \frac{\bar{S}^2 \mu_s \tilde{\mu}_s}{fc \bar{S} \mu_s \xi + \bar{S}_v f^2 cc_v \xi} \left(\frac{\bar{S}_v f^2 cc_v \xi}{\tilde{\mu}_s \bar{S} (\alpha_1 + \mu_1)} - 1 \right), \end{aligned}$$

and since $\tilde{\mu}_s = \tilde{\mu}$ this can be rewritten

$$I_1 = \frac{\bar{S}^2 \mu_s \tilde{\mu}_s (R_0^2 - 1)}{fc \bar{S} \mu_s \xi + \bar{S}_v f^2 cc_v \xi}.$$

Thus we only have a nonzero equilibrium when $R_0 \neq 1$, and when $R_0 < 1$ the nonzero equilibrium is negative, and when $R_0 > 1$ there is one endemic equilibrium. The content of the above discussion is contained in the following theorem:

Theorem 2. *Given a simple vector-borne relapsing disease model 2.1, 2.2, for every value of $R_0 > 1$ there is exactly one nonzero EE. For R_0 sufficiently close to 1, this EE is locally asymptotically stable.*

The form of the EE is complicated so evaluating the Jacobian at the EE is a difficult problem, and thus so is determining their stability away from $R_0 = 1$. The most efficient way to determine the stability of the EE is with Lyapunov functions (LF), though the standard LF for vector-borne diseases with no relapses in [20] did not yield any results. The LF in [9] could potentially be extended to this case.

6 Removal to the Recovered Compartment

In TBRF there can be some variation in the number of relapses experienced by infected hosts. We introduce this variation into our model by allowing individuals to leave an infected compartment and go directly to the recovered state. This can also correspond to treatment of the disease at that particular compartment. Let $\theta_i \geq 0$ be the transfer rate to the recovered compartment out of the

i th infected compartment. The equations change only slightly: the μ_i get replaced with $\mu_i + \theta_i$ and the recovered equation changes.

$$\begin{aligned}
S' &= \beta(N) - fc_v \tilde{I} \frac{S}{N} - \mu_s S, \\
I'_1 &= fc_v \tilde{I} \frac{S}{N} - \alpha_1 I_1 - (\mu_1 + \theta_1) I_1, \\
I'_2 &= \alpha_1 I_1 - \alpha_2 I_2 - (\mu_2 + \theta_2) I_2, \\
&\vdots \\
I'_{j-1} &= \alpha_{j-2} I_{j-2} - \alpha_{j-1} I_{j-1} - (\mu_{j-1} + \theta_{j-1}) I_{j-1}, \\
I'_j &= \alpha_{j-1} I_{j-1} - \gamma I_j - \mu_j I_j, \\
R' &= \sum_{i=1}^{j-1} \theta_i I_i + \gamma I_j - \mu_r R.
\end{aligned} \tag{6.1}$$

The vector equations remain unchanged:

$$\begin{aligned}
\tilde{S}' &= \beta_v(\tilde{N}, N) - \frac{fc\tilde{S}}{N} \sum_{k=1}^j I_k - \tilde{\mu}_s \tilde{S}, \\
\tilde{I}' &= \frac{fc\tilde{S}}{N} \sum_{k=1}^j I_k - \tilde{\mu} \tilde{I}.
\end{aligned} \tag{6.2}$$

Under the assumption that the population is constant ($N = \bar{S}$) we sum these equations to get

$$0 = N' = \beta(\bar{S}) - \sum_{i=1}^{j-1} \mu_i I_i - \gamma I_j - \mu_r R,$$

and following the proof of Proposition 1 in the Appendix we get that all the $\mu_i = \mu_r = \mu_s$. Similarly, if we assume $\mu_i = \mu_r = \mu_s$, then we have that $N = \bar{S}$ is invariant.

It is straightforward to show that this system satisfies the necessary conditions for the use of the next generation method.

Proposition 3. *The system (6.1), (6.2) satisfies Conditions 1-5.*

The proof is done in the exact same way as in Appendix A.1.

Now we move ahead to compute R_0 . However, note that this process involves only the infected equations and not the recovered equation. So the process is exactly the same as in the last section, but with μ_i replaced by $\mu_i + \theta_i$. Thus when we have removal to the recovered compartment:

$$R_0 = f \sqrt{\frac{cc_v \bar{S}_v}{\tilde{\mu} \bar{S}} \frac{1}{\alpha_1 + \mu_1 + \theta_1} \left(1 + \frac{\alpha_1}{\alpha_2 + \mu_2 + \theta_2} \left(1 + \frac{\alpha_2}{\alpha_3 + \mu_3 + \theta_3} \left(1 + \dots \frac{\alpha_{j-2}}{\alpha_{j-1} + \mu_{j-1} + \theta_{j-1}} \left(1 + \frac{\alpha_{j-1}}{\gamma + \mu_j} \right) \dots \right) \right) \right)}.$$

Alternatively,

$$R_0 = f \sqrt{\frac{cc_v \bar{S}_v}{\tilde{\mu} \bar{S}} \sum_{k=1}^j \prod_{l=1}^k \frac{\alpha_{l-1}}{\alpha_l + \mu_l + \theta_l}} \tag{6.3}$$

where $\alpha_0 = 1$ and $\alpha_j = \gamma$. As one might expect, removal to the recovered compartment drives down R_0 since the $\theta_i \geq 0$ only appear in the denominators. The magnitude of this contribution is determined by the size of θ_i compared to α_{i-1} . If the recovery rate from the i th compartment is small compared to the rate at which individuals are being transferred into that compartment, then it has little effect on the spread of the disease. Conversely, if the direct recovery from the i th infected compartment is large compared to the rate at which individuals are transferred in, it will result in a more significant mitigation of the disease spread.

We can also use this result to determine at which stage treatment of the disease is most effective, in terms of reducing R_0 . Treatment at the i th compartment is equivalent to increasing θ_i , which then reduces the size of the terms in the sum in Equation (6.3) for $k \geq i$. Hence, the compartment that reduces the most terms yields the largest decrease in R_0 i.e. the first compartment. This matches our intuition, since we most drastically reduce total infection time, and thus the ability of the host to infect a susceptible vector, by treating the disease before the first relapse.

6.1 The Bifurcation at $R_0 = 1$

There are still questions about which results from the previous section are easily extended to the case with removal to the recovered compartment, e.g., the transcritical bifurcation at $R_0 = 1$ and the number of EE. As an opening step we consider the Jacobian matrix for this system:

$$\begin{pmatrix} \alpha_1 + \mu_1 + \theta_1 & 0 & 0 & \dots & 0 & 0 & -fc_v & 0 & 0 & 0 \\ -\alpha_1 & \alpha_2 + \mu_2 + \theta_2 & 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\alpha_2 & \alpha_3 + \mu_3 + \theta_3 & \dots & 0 & 0 & 0 & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & -\alpha_{j-1} & \gamma + \mu_j & 0 & 0 & 0 & 0 \\ -\frac{fc\tilde{S}_v}{\tilde{S}} & -\frac{fc\tilde{S}_v}{\tilde{S}} & -\frac{fc\tilde{S}_v}{\tilde{S}} & \dots & -\frac{fc\tilde{S}_v}{\tilde{S}} & -\frac{fc\tilde{S}_v}{\tilde{S}} & \tilde{\mu} & 0 & 0 & 0 \\ 0 & 0 & 0 & \dots & 0 & 0 & fc_v & \mu_s & 0 & 0 \\ \frac{fc\tilde{S}}{N} & \frac{fc\tilde{S}}{N} & \frac{fc\tilde{S}}{N} & \dots & \frac{fc\tilde{S}}{N} & \frac{fc\tilde{S}}{N} & 0 & 0 & \tilde{\mu}_s & 0 \\ -\theta_1 & -\theta_2 & -\theta_3 & \dots & -\theta_{j-1} & -\gamma & 0 & 0 & 0 & \mu_r \end{pmatrix}$$

To apply Theorem 1 we need to know the multiplicity for the 0 eigenvalue for this matrix. The simplicity of the 0 eigenvalue and the proof that $b \neq 0$ (as defined in the previous sections) are precisely the same here as in Appendix A.2. While we now have more nonzero elements in $-J_4^{-1}J_3$, the $\epsilon_{3,k}$, are cancelled out since the associated second derivatives in the equation for a are the derivative of an infected variable with respect to the recovered variable, and thus are 0. Thus, the computation for a is exactly the same as Appendix A.3 and we have $a < 0$. Hence, we have the following Corollary:

Corollary 1. *The nontrivial DFE of the system (6.1), (6.2) undergoes a transcritical bifurcation as R_0 goes above 1, and has a branch of locally asymptotically stable EE for R_0 sufficiently close to 1.*

7 Discussion and Future Work

Using the next generation method and standard matrix computation methods we have found a form for R_0 of vector-borne relapsing diseases with an arbitrary number of relapses. From this

we conclude that R_0 increases as the number of relapses of the disease increases, with all other parameters fixed. We have also taken advantage of results in [23] to show the existence of a branch of endemic equilibria that are locally asymptotically stable for R_0 sufficiently close to 1. A straightforward calculation demonstrated that only one such branch of endemic equilibria can exist. Both of these results are independent of the number of relapses. The form of R_0 did not yield any particularly enlightening control strategies for the disease: R_0 can be completely controlled through, biting rate, competencies, population size, and vector death rates.

The computation of R_0 relied on the assumption of a constant population in the hosts. This assumption was shown to be equivalent to equal death rates in the infected host compartments. Allowing for variable death rates among the compartments changes the form of the Jacobians that make up the next generation matrix, though future work may show that the computations for R_0 are similar. However, in the case of equal death rates the constant population is found to be attracting and thus we need only study the dynamics restricted to this constant population.

Future work will consider refinements of our model which incorporate a period of non-infectivity (a latent state) in the hosts between relapses. The relapses of TBRF are driven by antigenic variation of *Borellia* spirochetes within the host [4]. Preceding this change is the host's immune response which nearly eradicates the bacteria from the host. However, *Borellia* can initiate a full infection with a single spirochete. Further details on the relapse mechanism can be found in [4]. The apparent lack of spirochetes in the host results in a week of apparent health between relapses of TBRF and any susceptible tick that bites the host will not become infected. Hence, hosts in this latent state will not drive the infection of susceptible vectors. Further work is focusing on the changes in R_0 and the dynamics caused by the addition of latent states.

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A Appendix

A.1 The Theory of Compartmental Models

We give a brief description of compartmental models here, following their development in [23]. Consider a population which can be separated into n homogeneous compartments, with the number of members in each compartment represented by the vector $\mathbf{x} \in \mathbb{R}^n$. We suppose that the first m compartments represent infected states while the remaining $n - m$ compartments are uninfected states. It is natural to insist that $\mathbf{x} \geq \mathbf{0}$ (inequality taken componentwise) since the x_i represent populations. Let $\mathbf{X}_s = \{\mathbf{x} \geq \mathbf{0} : x_i = 0, i = 1, \dots, m\}$ be the disease free states. Let $\mathcal{F}_i(\mathbf{x})$ be the number of new infections in compartment i (autonomy is assumed). $\mathcal{V}_i^+(\mathbf{x})$ is the rate of transfer of individuals into compartment i and $\mathcal{V}_i^-(\mathbf{x})$ is the rate of transfer out. Assume that these function are at least twice continuously differentiable and we can write our disease transmission model as

$$\dot{x}_i = f_i(\mathbf{x}) = \mathcal{F}_i(\mathbf{x}) + \mathcal{V}_i^+(\mathbf{x}) - \mathcal{V}_i^-(\mathbf{x}) \quad i = 1, \dots, n \quad (\text{A.1})$$

Five conditions need to be met in order to split the system in such a way that the computation of R_0 is straightforward. They are as follows.

$$\textcircled{1} \quad \mathbf{x} \geq \mathbf{0} \Rightarrow \mathcal{F}_i, \mathcal{V}_i^+, \mathcal{V}_i^- \geq 0$$

This is natural to assume as these functions represent a transfer of individuals between compartments.

$$\textcircled{2} \quad x_i = 0 \Rightarrow \mathcal{V}_i^-(\mathbf{x}) = 0$$

This condition requires that no individuals can transfer out of an empty compartment. In particular, if we are in \mathbf{X}_s then we have $\mathcal{V}_i = 0$ for $i = 1, 2, \dots, m$. These two conditions are enough to prove that solutions of the ODE will remain nonnegative when the initial conditions are nonnegative.

$$\textcircled{3} \quad \mathcal{F}_i = 0 \text{ for } i > m$$

Hence there are no new infections in the noninfected compartments.

$$\textcircled{4} \quad \mathbf{x} \in \mathbf{X}_s \Rightarrow \mathcal{F}_i(\mathbf{x}) = 0 \text{ and } \mathcal{V}_i^+(\mathbf{x}) = 0 \text{ for } i = 1, \dots, m$$

This condition insures that in disease free states there are no new infections in the infected compartments and there are no individuals being transferred into those compartments. Now assume that $\mathbf{x}_0 \in \mathbf{X}_s$ is a fixed point of (A.1). Such points are called Disease Free Equilibria (DFE). We consider only systems where DFE are stable in the absence of infection. Let $\mathcal{F}(\mathbf{x}) = (\mathcal{F}_1(\mathbf{x}), \dots, \mathcal{F}_n(\mathbf{x}))^T$ then

$$\textcircled{5} \quad \mathcal{F}(\mathbf{x}) \equiv \mathbf{0} \Rightarrow \text{The DFE is stable.}$$

In particular this implies that the Jacobian $Df(\mathbf{x}_0)$ has eigenvalues with negative real parts. Let $\mathcal{V}_i = \mathcal{V}_i^- - \mathcal{V}_i^+$ and $\mathcal{V} = (\mathcal{V}_1, \dots, \mathcal{V}_n)^T$. Then $f = \mathcal{F} - \mathcal{V}$. It can be shown that

$$Df(\mathbf{x}_0) = D\mathcal{F}(\mathbf{x}_0) - D\mathcal{V}(\mathbf{x}_0) = \begin{pmatrix} F & 0 \\ 0 & 0 \end{pmatrix} - \begin{pmatrix} V & 0 \\ J_3 & J_4 \end{pmatrix}$$

The $n \times n$ matrix F is nonnegative, the $n \times n$ matrix V is nonsingular and J_4 has eigenvalues with positive real parts. The matrix FV^{-1} is called the next generation matrix. Theorem 2 of [23] says that given a system (A.1) satisfying Conditions 1-5, if $\rho(FV^{-1}) < 1$ the DFE is asymptotically stable, and if $\rho(FV^{-1}) > 1$ the DFE is unstable. We confirm now that our model meets the conditions.

Proposition 4. *The system (2.1), (2.2) satisfies conditions 1-5.*

Proof. Rearrange the system into a vector with the infected hosts, infected vectors, susceptible host recovered host, and susceptible vector :

$$\frac{d}{dt} \begin{pmatrix} I_1 \\ I_2 \\ \vdots \\ I_{j-1} \\ I_j \\ \tilde{I} \\ S \\ R \\ \tilde{S} \end{pmatrix} = \begin{pmatrix} fc_v \tilde{I} \frac{S}{N} \\ 0 \\ \vdots \\ 0 \\ 0 \\ \frac{fc\tilde{S}}{N} \sum_{k=1}^j I_k \\ 0 \\ 0 \\ 0 \end{pmatrix} + \begin{pmatrix} 0 \\ \alpha_1 I_1 \\ \vdots \\ \alpha_{j-2} I_{j-2} \\ \alpha_{j-1} I_{j-1} \\ 0 \\ \beta(N) \\ \beta(N, \tilde{N}) \\ \gamma I_j \end{pmatrix} - \begin{pmatrix} (\alpha_1 + \mu_1) I_1 \\ (\alpha_2 + \mu_2) I_2 \\ \vdots \\ (\alpha_{j-1} + \mu_{j-2}) I_{j-2} \\ (\alpha_{j-1} + \mu_{j-1}) I_{j-1} \\ (\gamma + \mu_j) I_j \\ \tilde{\mu} \tilde{I} \\ fc_v \tilde{I} \frac{S}{N} + \mu_s S \\ \frac{fc\tilde{S}}{N} \sum_{k=1}^j I_k + \tilde{\mu}_s \tilde{S} \\ \mu_r R \end{pmatrix} \quad (\text{A.2})$$

Once we have written the system in the form (A.1), conditions 1,2 and 3 follow directly from this form. Setting $I_1 = \dots = I_j = \tilde{I} = 0$ gives condition 4. For the final condition, assume that the first vector on the right hand side of the above equation is $\mathbf{0}$. Then, taking the Jacobian will yield a lower triangular matrix, because each equation does not involve a variable beyond its row. Furthermore, the elements of the diagonal of this matrix, when evaluated at a DFE $(0, \dots, 0, \bar{S}, \bar{R}, \bar{S}_v)$, are

$$-(\alpha_1 + \mu_1), \dots, -(\alpha_{j-1} + \mu_{j-1}), -(\gamma + \mu_j), -\tilde{\mu}, -\mu_s, -\mu_r, -\tilde{\mu}_s$$

and as all the parameters are held to be positive, the diagonal elements, which are also the eigenvalues, are negative. \square

A.2 Simplicity of the 0 eigenvalue.

Consider the system (A.1). It is an easy exercise to show that the Jacobian of (A.1) takes the form

$$\begin{pmatrix} -\alpha_1 - \mu_1 & 0 & 0 & \dots & 0 & 0 & \frac{fc_v S}{N} & 0 & 0 & 0 \\ \alpha_1 & -\alpha_2 - \mu_2 & 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \alpha_2 & -\alpha_3 - \mu_3 & \dots & 0 & 0 & 0 & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & \alpha_{j-1} & -\gamma - \mu_j & 0 & 0 & 0 & 0 \\ \frac{fc\tilde{S}}{N} & \frac{fc\tilde{S}}{N} & \frac{fc\tilde{S}}{N} & \dots & \frac{fc\tilde{S}}{N} & \frac{fc\tilde{S}}{N} & -\tilde{\mu} & 0 & 0 & 0 \\ 0 & 0 & 0 & \dots & 0 & 0 & -\frac{fc_v S}{N} & -\mu_s & 0 & 0 \\ -\frac{fc\tilde{S}}{N} & -\frac{fc\tilde{S}}{N} & -\frac{fc\tilde{S}}{N} & \dots & -\frac{fc\tilde{S}}{N} & -\frac{fc\tilde{S}}{N} & 0 & 0 & -\tilde{\mu}_s & 0 \\ 0 & 0 & 0 & \dots & 0 & \gamma & 0 & 0 & 0 & -\mu_r \end{pmatrix}$$

We evaluate this at the DFE and then determine the algebraic multiplicity of the zero eigenvalue when $R_0 = 1$. The eigenvalue matrix is

$$\begin{pmatrix} \lambda + \alpha_1 + \mu_1 & 0 & 0 & \dots & 0 & 0 & -fc_v & 0 & 0 & 0 \\ -\alpha_1 & \lambda + \alpha_2 + \mu_2 & 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\alpha_2 & \lambda + \alpha_3 + \mu_3 & \dots & 0 & 0 & 0 & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & -\alpha_{j-1} & \lambda + \gamma + \mu_j & 0 & 0 & 0 & 0 \\ -\frac{fc\tilde{S}_v}{S} & -\frac{fc\tilde{S}_v}{S} & -\frac{fc\tilde{S}_v}{S} & \dots & -\frac{fc\tilde{S}_v}{S} & -\frac{fc\tilde{S}_v}{S} & \lambda + \tilde{\mu} & 0 & 0 & 0 \\ 0 & 0 & 0 & \dots & 0 & 0 & fc_v & \lambda + \mu_s & 0 & 0 \\ \frac{fc\tilde{S}}{N} & \frac{fc\tilde{S}}{N} & \frac{fc\tilde{S}}{N} & \dots & \frac{fc\tilde{S}}{N} & \frac{fc\tilde{S}}{N} & 0 & 0 & \lambda + \tilde{\mu}_s & 0 \\ 0 & 0 & 0 & \dots & 0 & -\gamma & 0 & 0 & 0 & \lambda + \mu_r \end{pmatrix}$$

The Jacobian matrix has block form

$$Df(\mathbf{x}_0) = \begin{pmatrix} T & 0 \\ L & D \end{pmatrix}$$

and the multiplicity of the zero eigenvalue will be the sum of the multiplicities of the diagonal blocks [2]. However, the multiplicity of 0 in D is 0, since it is diagonal. Hence we need only compute the multiplicity of zero in T . The relevant calculation is

$$p(\lambda) = \det \begin{pmatrix} \lambda + \alpha_1 + \mu_1 & 0 & 0 & \dots & 0 & 0 & -fc_v \\ -\alpha_1 & \lambda + \alpha_2 + \mu_2 & 0 & \dots & 0 & 0 & 0 \\ 0 & -\alpha_2 & \lambda + \alpha_3 + \mu_3 & \dots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & -\alpha_{j-1} & \lambda + \gamma + \mu_j & 0 \\ -\frac{fc\tilde{S}_v}{S} & -\frac{fc\tilde{S}_v}{S} & -\frac{fc\tilde{S}_v}{S} & \dots & -\frac{fc\tilde{S}_v}{S} & -\frac{fc\tilde{S}_v}{S} & \lambda + \tilde{\mu} \end{pmatrix}$$

First we expand along the top row

$$p(\lambda) = (\lambda + \alpha_1 + \mu_1) \det \begin{pmatrix} \lambda + \alpha_2 + \mu_2 & 0 & \dots & 0 & 0 & 0 \\ -\alpha_2 & \lambda + \alpha_3 + \mu_3 & \dots & 0 & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & \dots & -\alpha_{j-1} & \lambda + \gamma + \mu_j & 0 \\ -\frac{fc\bar{S}_v}{\bar{S}} & -\frac{fc\bar{S}_v}{\bar{S}} & \dots & -\frac{fc\bar{S}_v}{\bar{S}} & -\frac{fc\bar{S}_v}{\bar{S}} & \lambda + \tilde{\mu} \end{pmatrix}$$

$$+ (-1)^j (-fc_v) \det \begin{pmatrix} -\alpha_1 & \lambda + \alpha_2 + \mu_2 & 0 & \dots & 0 & 0 \\ 0 & -\alpha_2 & \lambda + \alpha_3 + \mu_3 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & -\alpha_{j-1} & \lambda + \gamma + \mu_j \\ -\frac{fc\bar{S}_v}{\bar{S}} & -\frac{fc\bar{S}_v}{\bar{S}} & -\frac{fc\bar{S}_v}{\bar{S}} & \dots & -\frac{fc\bar{S}_v}{\bar{S}} & -\frac{fc\bar{S}_v}{\bar{S}} \end{pmatrix}$$

The determinant of the first matrix is the product of the diagonals, being that it is lower triangular. Computing the second determinant requires some courage, and a little trickiness. First we divide the bottom row by $-\frac{fc\bar{S}_v}{\bar{S}}$. For the value of the determinant to stay the same, we also multiply it by the same amount. Hence we compute

$$(-1)^j \frac{f^2 cc_v \bar{S}_v}{\bar{S}} \det \begin{pmatrix} -\alpha_1 & \lambda + \alpha_2 + \mu_2 & 0 & \dots & 0 & 0 \\ 0 & -\alpha_2 & \lambda + \alpha_3 + \mu_3 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & -\alpha_{j-1} & \lambda + \gamma + \mu_j \\ 1 & 1 & 1 & \dots & 1 & 1 \end{pmatrix}$$

by expanding along the bottom row. Then at each step of the expansion we will take the determinant of a block diagonal matrix, and each matrix along the diagonal will be a triangular matrix. In particular, once the k th column and the bottom row are removed, the diagonal to the left of the column has the elements $-\alpha_1, \dots, -\alpha_{k-1}$ with the only other nonzero elements above this diagonal. To the right of the column the diagonal elements are $\lambda + \alpha_{k+1} + \mu_{k+1}, \dots, \lambda + \gamma + \mu_j$, and on this side the only other nonzero elements are above the diagonal. Thus the minors can be written in this form

$$\begin{pmatrix} A & 0 \\ 0 & B \end{pmatrix}$$

According to [2] the determinant of this minor will be the product of the determinants of the diagonal matrices, and as we have already mentioned A is upper triangular and B is lower triangular. Thus, the determinant of the minor is the product of the diagonal elements. The signs for the minors along the bottom are $(-1)^{j+k}$. Furthermore we will multiply the $k-1$ negative elements in the upper matrix. Hence the sign of each term is $(-1)^{j+k+k-1} = (-1)^{j+2k-1} = (-1)^{j-1}$. None of these depend on k , we can factor it out and combine it with the $(-1)^j$ on the outside, and have

$(-1)^{j+j-1} = -1$. Thus, the characteristic polynomial takes the form

$$\begin{aligned} p(\lambda) = & (\lambda + \alpha_1 + \mu_1) \dots (\lambda + \gamma + \mu_j)(\lambda + \tilde{\mu}) \\ & - \frac{f^2 cc_v \bar{S}_v}{\bar{S}} [(\lambda + \alpha_2 + \mu_2) \dots (\lambda + \gamma + \mu_j) \\ & + \alpha_1(\lambda + \alpha_3 + \mu_3) \dots (\lambda + \gamma + \mu_j) \\ & + \dots \alpha_1 \dots \alpha_k(\lambda + \alpha_{k+2} + \mu_{k+2}) \dots (\lambda + \gamma + \mu_j) + \dots + \alpha_1 \dots \alpha_{j-1}] \end{aligned}$$

To show that 0 is a simple eigenvalue, we must show that when $R_0 = 1$, the constant term of this polynomial is 0 and the linear term is nonzero. In order to ease some of the calculation we next build up some notation. For indexing purposes define $\alpha_0 = 1$. Now let $\xi_i = \alpha_i + \mu_i$ for $1 \leq i \leq j-1$ and $\xi_j = \gamma + \mu_j$ and $\xi_{j+1} = \tilde{\mu}$. This sets up a consistent notation for the parameters. Also, we need to take products of all but one of these parameters, so we define the following

$$\xi_1 \dots \hat{\xi}_i \dots \xi_j = \xi_1 \dots \xi_{i-1} \xi_{i+1} \dots \xi_j$$

The hat tells us which of the parameters is deleted from the product. We can now rewrite R_0 using this notation

$$R_0 = f \sqrt{\frac{cc_v \bar{S}_v}{\bar{S} \xi_{j+1}} \sum_{k=1}^j \frac{\alpha_0 \dots \alpha_{k-1}}{\xi_1 \dots \xi_k}}$$

and $p(\lambda)$ becomes

$$p(\lambda) = \prod_{i=1}^j (\lambda + \xi_i) - \frac{f^2 cc_v \bar{S}_v}{\bar{S}} \sum_{i=0}^{j-1} \alpha_0 \dots \alpha_i (\lambda + \xi_{i+2}) \dots (\lambda + \xi_j) \quad (\text{A.3})$$

The constant term is found by evaluating $p(0)$:

$$p(0) = \prod_{i=1}^j \xi_i - \frac{f^2 cc_v \bar{S}_v}{\bar{S}} \sum_{i=0}^{j-1} \alpha_0 \dots \alpha_i \xi_{i+2} \dots \xi_j$$

Next, we solve $p(0) = 0$.

$$\begin{aligned} 1 &= \frac{f^2 cc_v \bar{S}_v}{\bar{S}} \frac{1}{\xi_1 \dots \xi_j \xi_{j+1}} \sum_{i=0}^{j-1} \alpha_0 \dots \alpha_i \xi_{i+2} \dots \xi_j \\ &= \frac{f^2 cc_v \bar{S}_v}{\bar{S} \xi_{j+1}} \sum_{i=0}^{j-1} \frac{\alpha_0 \dots \alpha_i \xi_{i+2} \dots \xi_j}{\xi_1 \dots \xi_j} \\ &= \frac{f^2 cc_v \bar{S}_v}{\bar{S} \xi_{j+1}} \sum_{i=0}^{j-1} \frac{\alpha_0 \dots \alpha_i}{\xi_1 \dots \xi_{i+1}} \end{aligned}$$

Letting $k = i + 1$ this becomes

$$= \frac{f^2 cc_v \bar{S}_v}{\bar{S} \xi_{j+1}} \sum_{k=1}^j \frac{\alpha_0 \dots \alpha_{k-1}}{\xi_1 \dots \xi_k} = R_0^2$$

This implies that the linear term is 0 if and only if $R_0 = 1$. This only establishes that the 0 has nontrivial algebraic multiplicity, to establish simplicity we check that the coefficient of the linear term is nonzero when $R_0 = 1$. Given a product of factors

$$(\lambda + a_1) \dots (\lambda + a_n)$$

the coefficient of the linear term, in the “hat” notation, is

$$\sum_{i=1}^n a_1 \dots \hat{a}_i \dots a_n$$

Applying this to (A.3) we find the coefficient of the linear term of the characteristic polynomial to be

$$\sum_{i=1}^{j+1} \xi_1 \dots \hat{\xi}_i \dots \xi_{j+1} - \frac{f^2 c c_v \bar{S}_v}{\bar{S}} \sum_{k=0}^{j-2} \alpha_0 \dots \alpha_k \sum_{i=k+2}^j \xi_{k+2} \dots \hat{\xi}_i \dots \xi_j$$

Assume that this is equal to zero when $R_0 = 1$ and we will arrive at a contradiction. Multiplying the second term by $\frac{\xi_{j+1}}{\xi_{j+1}}$

$$0 = \sum_{i=1}^{j+1} \xi_1 \dots \hat{\xi}_i \dots \xi_{j+1} - \frac{f^2 c c_v \bar{S}_v}{\bar{S} \xi_{j+1}} \sum_{k=0}^{j-2} \sum_{i=k+2}^j \alpha_0 \dots \alpha_k \xi_{k+2} \dots \hat{\xi}_i \dots \xi_j \xi_{j+1}$$

where upon some manipulation the expression yields

$$1 = \frac{\frac{f^2 c c_v \bar{S}_v}{\bar{S} \xi_{j+1}} \sum_{k=0}^{j-2} \sum_{i=k+2}^j \alpha_0 \dots \alpha_k \xi_{k+2} \dots \hat{\xi}_i \dots \xi_j \xi_{j+1}}{\sum_{i=1}^{j+1} \xi_1 \dots \hat{\xi}_i \dots \xi_{j+1}}$$

But $R_0^2 = 1$ so

$$\frac{f^2 c c_v \bar{S}_v}{\bar{S} \xi_{j+1}} \sum_{k=1}^j \frac{\alpha_0 \dots \alpha_{k-1}}{\xi_1 \dots \xi_k} = \frac{\frac{f^2 c c_v \bar{S}_v}{\bar{S} \xi_{j+1}} \sum_{k=0}^{j-2} \sum_{i=k+2}^j \alpha_0 \dots \alpha_k \xi_{k+2} \dots \hat{\xi}_i \dots \xi_j \xi_{j+1}}{\sum_{i=1}^{j+1} \xi_1 \dots \hat{\xi}_i \dots \xi_{j+1}}$$

Canceling the constant in front, and multiplying by the denominator we get

$$\sum_{i=1}^j \sum_{k=1}^{j+1} \frac{\alpha_0 \dots \alpha_{i-1} \xi_1 \dots \hat{\xi}_k \dots \xi_{j+1}}{\xi_1 \dots \xi_i} = \sum_{k=0}^{j-2} \sum_{i=k+2}^j \alpha_0 \dots \alpha_k \xi_{k+2} \dots \hat{\xi}_i \dots \xi_j \xi_{j+1}$$

We can split the first sum into two parts depending on the largest value of k . In particular, when $k \leq i$ ξ_k will not cancel out of the denominator, but when $k \geq i + 1$ the whole denominator will

cancel, so we write

$$\begin{aligned} \sum_{i=1}^j \sum_{k=1}^i \frac{\alpha_0 \dots \alpha_{i-1} \xi_{i+1} \dots \xi_{j+1}}{\xi_k} + \sum_{i=1}^j \sum_{k=i+1}^j \alpha_0 \dots \alpha_{i-1} \xi_{i+1} \dots \hat{\xi}_k \dots \xi_{j+1} \\ = \sum_{k=0}^{j-2} \sum_{i=k+2}^j \alpha_0 \dots \alpha_k \xi_{k+2} \dots \hat{\xi}_i \dots \xi_j \xi_{j+1} \end{aligned}$$

Exchanging i and k on the right hand side this becomes

$$\begin{aligned} \sum_{i=1}^j \sum_{k=1}^i \frac{\alpha_0 \dots \alpha_{i-1} \xi_{i+1} \dots \xi_{j+1}}{\xi_k} + \sum_{i=1}^j \sum_{k=i+1}^j \alpha_0 \dots \alpha_{i-1} \xi_{i+1} \dots \hat{\xi}_k \dots \xi_{j+1} \\ = \sum_{i=0}^{j-2} \sum_{k=i+2}^j \alpha_0 \dots \alpha_i \xi_{i+2} \dots \hat{\xi}_k \dots \xi_j \xi_{j+1} \end{aligned}$$

Shifting the i index up by 1 on the RHS yields

$$\begin{aligned} \sum_{i=1}^j \sum_{k=1}^i \frac{\alpha_0 \dots \alpha_{i-1} \xi_{i+1} \dots \xi_{j+1}}{\xi_k} + \sum_{i=1}^j \sum_{k=i+1}^j \alpha_0 \dots \alpha_{i-1} \xi_{i+1} \dots \hat{\xi}_k \dots \xi_{j+1} \\ = \sum_{i=1}^{j-1} \sum_{k=i+1}^j \alpha_0 \dots \alpha_{i-1} \xi_{i+1} \dots \hat{\xi}_k \dots \xi_j \xi_{j+1} \end{aligned}$$

Thus we have that

$$\sum_{i=1}^j \sum_{k=1}^i \frac{\alpha_0 \dots \alpha_{i-1} \xi_{i+1} \dots \xi_{j+1}}{\xi_k} + \alpha_0 \dots \alpha_{j-1} = 0$$

However, this cannot be so because all of the rates are positive. Hence a contradiction and the conclusion that the linear term cannot be 0 when $R_0 = 1$, and 0 is a simple eigenvalue of $Df(x_0)$.

A.3 Proof of Lemma 1

First note that the last three components of v are 0. This follows from the fact that

$$J_4 = \begin{pmatrix} \mu_s & 0 & 0 \\ 0 & \tilde{\mu}_s & 0 \\ 0 & 0 & \mu_r \end{pmatrix}$$

is invertible. Because

$$f = \frac{\mu + 1}{\zeta},$$

the only nonzero derivatives in the expression for b are in the I and \tilde{I} compartments, since these are the only ones that involve μ . As the last three components of v are 0, we have

$$b = v_1 \left(\sum_{k=1}^j w_k \frac{\partial f_1}{\partial I_k \partial \mu} + w_{j+1} \frac{\partial f_1}{\partial \tilde{I} \partial \mu} + w_{j+1} \frac{\partial f_1}{\partial S \partial \mu} + w_{j+3} \frac{\partial f_1}{\partial \tilde{S} \partial \mu} + w_{j+4} \frac{\partial f_1}{\partial R \partial \mu} \right)$$

$$+v_{j+1} \left(\sum_{k=1}^j w_k \frac{\partial f_{j+1}}{\partial I_k \partial \mu} + w_{j+1} \frac{\partial f_{j+1}}{\partial \tilde{I} \partial \mu} + w_{j+2} \frac{\partial f_{j+1}}{\partial S \partial \mu} + w_{j+3} \frac{\partial f_{j+1}}{\partial \tilde{S} \partial \mu} + w_{j+4} \frac{\partial f_{j+1}}{\partial R \partial \mu} \right)$$

Taking derivatives and evaluating at the DFE gives that

$$\begin{aligned} b &= v_1(0 + w_{j+1} \frac{c_v}{\zeta} + 0 + 0 + 0) + v_{j+1} \left(\sum_{k=1}^j w_k \frac{c \bar{S}_v}{\bar{S} \zeta} + 0 + 0 + 0 + 0 \right) \\ &= v_1 w_{j+1} \frac{c_v}{\zeta} + \frac{v_{j+1} c \bar{S}_v}{\bar{S} \zeta} \sum_{k=1}^j w_k \end{aligned}$$

We need to show that this is nonzero. First we claim that at least one of the w_i are nonzero. Suppose not, and that we have $w_1 = \dots = w_{j+1} = 0$. Then since $v_{j+2} = v_{j+3} = v_{j+4} = 0$,

$$vw = \sum_{i=1}^{j+4} v_i w_i = 0$$

which is a contradiction. Next we claim that $v_1 \neq 0$ or $v_{j+1} \neq 0$. Suppose to the contrary that $v_1 = v_{j+1} = 0$. Then because

$$(v_1, \dots, v_{j+1}, 0, 0, 0) Df(x_0) = 0$$

it follows that

$$\begin{aligned} &(0, v_2, \dots, v_j, 0, 0, 0) Df(x_0) = 0. \\ \Rightarrow (v_2, \dots, v_j) &\begin{pmatrix} \alpha_1 & -\alpha_2 - \mu_2 & \dots & 0 & 0 \\ \vdots & \ddots & \ddots & \vdots & \vdots \\ 0 & 0 & \vdots & -\alpha_{j-1} - \mu_{j-1} & 0 \\ 0 & 0 & \vdots & \alpha_{j-1} & -\gamma - \mu_j \end{pmatrix} = 0 \end{aligned}$$

The last column shows that $v_j = 0$, so the expression further reduces to

$$(v_2, \dots, v_{j-1}) \begin{pmatrix} \alpha_1 & -\alpha_2 - \mu_2 & \dots & 0 \\ \vdots & \ddots & \ddots & \vdots \\ 0 & 0 & \vdots & -\alpha_{j-1} - \mu_{j-1} \end{pmatrix} = 0$$

Again, the last column implies that $v_{j-1} = 0$, and so on. This means $v = 0$, but $vw = 1$, which is a contradiction. Then because all the terms in b are nonnegative, with some of them being nonzero, we arrive at $b \neq 0$.

To show that $a > 0$ note that

$$J_3 = \begin{pmatrix} 0 & \dots & 0 & f c_v \\ \frac{f c \bar{S}_v}{\bar{S}} & \dots & \frac{f c \bar{S}_v}{\bar{S}} & 0 \\ 0 & \dots & \gamma & 0 \end{pmatrix}$$

and

$$J_4^{-1} = \begin{pmatrix} \frac{1}{\mu_s} & 0 & 0 \\ 0 & \frac{1}{\tilde{\mu}_s} & 0 \\ 0 & 0 & \frac{1}{\mu_r} \end{pmatrix}$$

Thus

$$-J_4^{-1} J_3 = \begin{pmatrix} 0 & \dots & 0 & \frac{fc_v}{\mu_s} \\ \frac{fc\bar{S}_v}{\tilde{\mu}_s\bar{S}} & \dots & \frac{fc\bar{S}_v}{\tilde{\mu}_s\bar{S}} & 0 \\ 0 & \dots & \frac{1}{\mu_r} & 0 \end{pmatrix}$$

We can list the nonzero elements of this matrix : $\varepsilon_{1(j+1)}, \varepsilon_{21}, \dots, \varepsilon_{2j}, \varepsilon_{3j}$. The second derivatives of the infected components with respect to an infected variable are all zero, since one differentiation removes all of that infected variable. When differentiating with respect to an infected variable and an uninfected variable, the derivatives of the I_2 through I_j components will be zero as they contain no uninfected variables. The nonzero derivatives are

$$\frac{\partial^2 f_1}{\partial \tilde{I} \partial S} = \frac{fc_v}{\bar{S}}$$

$$\frac{\partial^2 f_{j+1}}{\partial I_k \partial \tilde{S}} = \frac{fc}{\bar{S}}$$

So then

$$\begin{aligned} a &= \sum_{i,j,k=1}^{j+1} v_i w_j w_k \left(0 - \frac{f^2 c_v^2}{\bar{S} \mu_s} - \sum_{l=1}^j \frac{f^2 c^2 \bar{S}_v}{\bar{S}^2 \tilde{\mu}_s} \right) \\ &= - \sum_{i,j,k=1}^{j+1} v_i w_j w_k \left(\frac{f^2 c_v^2}{\bar{S} \mu_s} + \frac{f^2 c^2 \bar{S}_v}{\bar{S}^2 \tilde{\mu}_s} \right) \end{aligned}$$

As we have already shown, the $v_i, w_i \geq 0$, and since the parameters are positive $a < 0$.